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A new species of *Hua* (Gastropoda, Semisulcospiridae) from Yunnan, southwest China

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Abstract

Species of the semisulcospirid freshwater gastropod *Hua* are mainly distributed in Guangxi, southwest China, and northern Vietnam, and are sensitive to water quality. The new species *Hua luquanensis* **sp. nov.** is described from southwest China, Yunnan Province, Kunming City, Luquan County, Zhuanlong Dragon Spring, based on morphological and molecular evidence. The new species is distinguished from its congeners by a combination of characters, including a smooth shell with 4–6 whorls, outer marginal radular teeth with 14 denticles, a body width of about 61.4–74.8% of shell height, and a large body whorl comprising about 79.8–91.7% of shell height.

Key Words

Cerithioidea, *Hua luquanensis* sp. nov., Jinsha River, taxonomy

Introduction

The freshwater gastropod family Semisulcospiridae is represented by three genera in China, viz. *Hua* Chen, 1943, *Koreoleptoxis* Burch and Jung, 1988, and *Semisulcospira* Boettger, 1886 (Du et al. 2019a, 2019b). The genus *Hua* was established by Chen (1943), with *Hua telonaria* (Heude, 1888) as the type species of *Hua*, collected from Takwan River (= Daguan River), Yunnan. Subsequently, 11 more species, including *H. diminuta* (Boettger, 1887), *H. friniana* (Heude, 1888), *H. hongkongiensis* (Brot, 1874), *H. joretiana* (Heude, 1890), *H. kweichowensis* (Chen, 1937), *H. leprosa* (Heude, 1890), *H. oreadarum* (Heude, 1888), *H. praenotata* (Gredler, 1884), *H. proteanura* (Bavay & Dautzenber, 1910), *H. schmackeri* (Boettger, 1886), *H. toucheana* (Heude, 1888), and *H. vultuosa* (Fulton, 1914), were also assigned to *Hua*. Morrison (1954) proposed to remove various species from *Hua* and place them in *Oxytrema* Rafinesque, 1819. However, this suggestion has not been accepted by subsequent authors, since the name *Oxytrema* was introduced for a North American taxon. Strong and Köhler (2009) provided the first detailed anatomical description for any Chinese species, in combination with the first molecular phylogenetic analysis. They showed that *Hua* is indeed distinct from *Semisulcospira* and characterized by distinct features of

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the digestive, reproductive, and nervous systems. More recently, Du et al. (2019a, 2019b) conducted a comprehensive revision of the systematics of Chinese Semisulcospiridae using both morphological characters and mitochondrial phylogenetics. The typical characters of *Hua* are being oviparous, mature females possessing an ovipositor pore, or egg-laying groove, below the right cephalic tentacle, and having one basal denticle in each lower outer corner of the central tooth of the radula (Du et al. 2019a).

Du et al. (2019b) placed *H. diminuta*, *H. friniana*, *H. hongkongiensis*, *H. joretiana*, *H. praenotata*, and *H. toucheana* in *Koreoleptoxis* and mentioned that species of *Hua* are limited in their distribution to streams and rivers of Guangxi and southwest China. Recently, Du and Yang (2023) described nine new species, namely *H. ovata* Du, Yang & Chen, 2023, *H. acris* Yang & Du, 2023, *H. pseudotextrix* Du, Yang & Chen, 2023, *H. qujingensis* Du, Yang & Chen, 2023, *H. wujiangensis* Du, Yang & Chen, 2023, *H. guipingensis* Du & Yang, 2023, *H. kaiyuanensis* Du & Yang, 2023, *H. shizongensis* Du, Yang & Chen, 2023, and *H. yangi* Du, Yang & Chen, 2023. In the same year, Chen et al. (2023) described *Hua qiannanensis* Chen, Shi, Du & Sun, 2023, from Guizhou, based on morphological characters and molecular evidence. Moreover, He et al. (2024) described 17 new species of Semisulcospiridae from southern China, including 12 new species of *Hua*, *H. yiliangensis* Lu, Chen & He, 2024, *H. rayeae* Lu, Chen & He, 2024, *H. yunong* Xiang, Chen & He, 2024, *H. heimao* Xiang, Chen & He, 2024, *H. jiuxiangensis* Fu, Chen & He, 2024, *H. penicillata* Chen & He, 2024, *H. wudangensis* Chen & He, 2024, *H. pyriformis* Chen & He, 2024, *H. censongyangi* Chen & He, 2024, *H. jundazhaoi* Chen & He, 2024, *H. jiahaojingi* Chen & He, 2024, and *H. mileensis* Chen & He, 2024. They also reinstated *Melania suifuensis* (Chen, 1937) as a valid species based on the shell morphology, radula, and operculum, and transferred it to the genus *Hua*. Currently, the genus *Hua* is known to comprise 38 described species, whose distributional range is confined to the provinces of Sichuan, Yunnan, Guizhou, and Guangxi in China, and northern Vietnam.

Specimens of a semisulcospirid species that can be assigned to the genus *Hua* were collected in Zhuanlong Dragon Spring, Luquan County, Kunming City, Yunnan Province, in April 2017. Based on morphological and molecular evidence, a comparison with other species of *Hua* revealed that it is an undescribed species. Although Du mentioned a new species, named *Hua luquanensis*, in her doctoral thesis, the species is not validly published. Additionally, this naked name was mentioned in He et al. (2024). Hence, this species is described here.

Materials and methods

Morphology

The following shell dimensions were measured with digital calipers accurate to 0.1 mm: H, shell height (maximum dimension parallel to the axis of coiling); B, shell width (maximum dimension perpendicular to H); LA, length of aperture (maximum dimension from the junction of the outer lip with the penultimate whorl to the anterior lip); WA, width of aperture (maximum dimension perpendicular to LA); BW, height of the last whorl (dimension from the lower margin of the aperture to the upper suture delimiting the first whorl). In addition, we counted the number of whorls, N. Radulae and embryonic shells were studied by scanning electron microscopy (SEM). Radulae were cleaned enzymatically with proteinase K as described by Holznagel (1998), sonicated, mounted on aluminum specimen stubs with adhesive tabs, and coated with gold–palladium to be studied with a HITACHI S-3000 scanning electron microscope at 15 kV. The descriptions of shell features follow Strong and Köhler (2009).

Molecular analyses

To support the generic placement of the new species, its phylogenetic position was investigated based on molecular data. Genomic DNA was extracted from foot tissue stored in 99% ethanol. Tissue samples were digested using proteinase K and subsequently purified following standard phenol/chloroform isolation and ethanol precipitation. Partial sequences of the mitochondrial cytochrome oxidase subunit I gene (COI, 772 bp) were amplified by PCR (Palumi et al. 1991) using the primers F2 (5'-TAAGYYTDYTAATTCGTGC-3') and R2 (5'-CGYGTRTCDACATCTATACCBACTG-3') (Du et al. 2019a) and subsequently sent for sequencing to Tsingke Biological Technology Company, Beijing, China. Muscle tissue (1 mm^3) was clipped from the foot of 54 additional samples for DNA extraction, and complete mitochondrial genomes were sequenced by Origingene Bio-Pharm Technology Co. Ltd., Shanghai, China. An E.Z.N.A.® Tissue DNA Kit (OMEGA Bio-tek, USA) was used to extract whole genomic DNA. The mitogenomes of *Hua* were sequenced using an Illumina TruSeq™ DNA Sample Preparation Kit (Illumina, San Diego, CA, USA) with paired reads measuring 300–500 bp in length. Quality control of raw genomic data was assessed using FastQC v.0.11.4. To evaluate the consistency of the assembly results, GetOrganelle (https://github.com/Kinggerm/GetOrganelle) and NOVOPlasty (https://github.com/ndierckx/NOVOPlasty) were used.

The molecular phylogenetic tree was reconstructed based on 59 newly generated COI sequences and 54 mitochondrial genomes produced in this study, together with 132 COI sequences and five mitochondrial genomes downloaded from GenBank (Suppl. material 1: table S1). Sequences of *Melanoides tuberculata* (Müller, 1774) and *Tarebia granifera* (Lamarck, 1822) were used as outgroups to root the phylogeny in accordance with the tree shown by Strong and

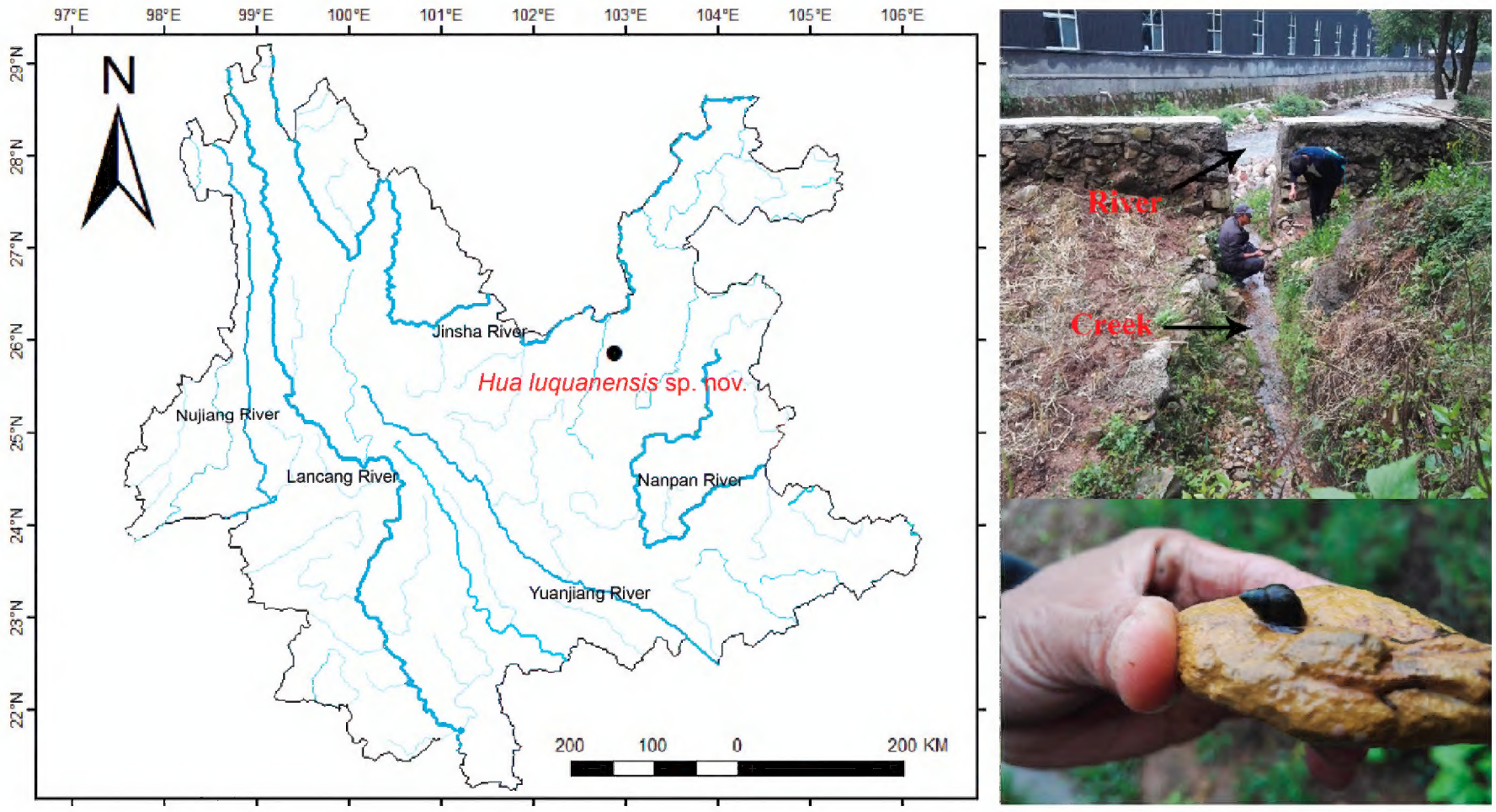

Figure 1. (**A**) Type locality in Yunnan, China, where *Hua luquanensis* sp. nov. was found (black triangle). (**B**) The habitat of *Hua luquanensis* sp. nov.

Köhler (2009). Sequences of COI and mitochondrial genomes obtained in the present study have been deposited in GenBank (for accession numbers, see Suppl. material 1: table S1).

Gene identification and extraction of thirteen protein-coding genes (COX1, COX2, COX3, CYTB, ND1, ND2, ND3, ND4, ND4L, ND5, ND6, ATP6, ATP8) were performed using the Biostrings package in the R environment (v4.4.1). For species possessing only COI barcode sequences (including the new species described in this study), their COI sequences were used directly. Each gene was individually aligned using MAFFT (Katoh and Standley 2013), with manual inspection of alignment quality and reading frame adjustment. Finally, aligned sequences from all genes were concatenated in a fixed order, resulting in a combined dataset of 16,490 bp for subsequent phylogenetic analyses. Phylogenetic relationships were reconstructed using the maximum likelihood method based on the concatenated sequences of 13 mitochondrial protein-coding genes and the COI gene. Tree construction was conducted using IQ-TREE v3.0.1 (Nguyen et al. 2015), with the optimal partitioning strategy determined by PartitionFinder (Lanfear et al. 2017) under the AICc criterion. The most suitable nucleotide substitution model was identified using the greedy search algorithm. Node support was evaluated using the ultrafast bootstrap method (Minh et al. 2013) with 1,000 replicates. The analysis was performed using four parallel threads, and all other parameters were set to default. The pairwise uncorrected p-distance between species was calculated in MEGA 7 (Kumar et al. 2016). The best substitution model was selected by employing the corrected Akaike Information Criterion (AICc) in jModelTest v2.1.10 (Posada 2008).

Results

Molecular data

A total of 224 mitochondrial sequences (including complete mitochondrial genomes and COI barcode sequences) from related species were utilized in the phylogenetic analyses. Based on the AICc criterion and greedy search algorithm, a final partition scheme consisting of seven subsets was selected (Table 1). The results indicated that the best-fit model for most gene partitions was GTR+I+G, including Partition 1 (ATP6, ND6, COX1, ND3), Partition 3 (ND4, CYTB, COX3), and Partition 4 (ND5, ND1), collectively covering 19,361 sites (79.9% of the total alignment). Partition 2 (COX2) was best modeled by HKY+G, while Partitions 5 (ND2), 6 (ND4L), and 7 (ATP8) were best fit by GTR+G. This partitioning scheme yielded an AICc score of 501,238.01, a log-likelihood of −250,096.98, and a total of 511 parameters.

Table 1. Nucleotide substitution model selection for gene partitions in *Hua luquanensis* sp. nov.

Partition	Best-fit model	Genes
1	GTR+I+G	ATP6, ND6, COX1, ND3
2	HKY+G	COX2
3	GTR+I+G	ND4, CYTB, COX3
4	GTR+I+G	ND5, ND1
5	GTR+G	ND2
6	GTR+G	ND4L
7	GTR+G	ATP8

Maximum likelihood analyses strongly supported placing the new species within its respective genus, forming a distinct clade with high bootstrap support (Fig. 2). Genetic distances calculated based on COI sequences

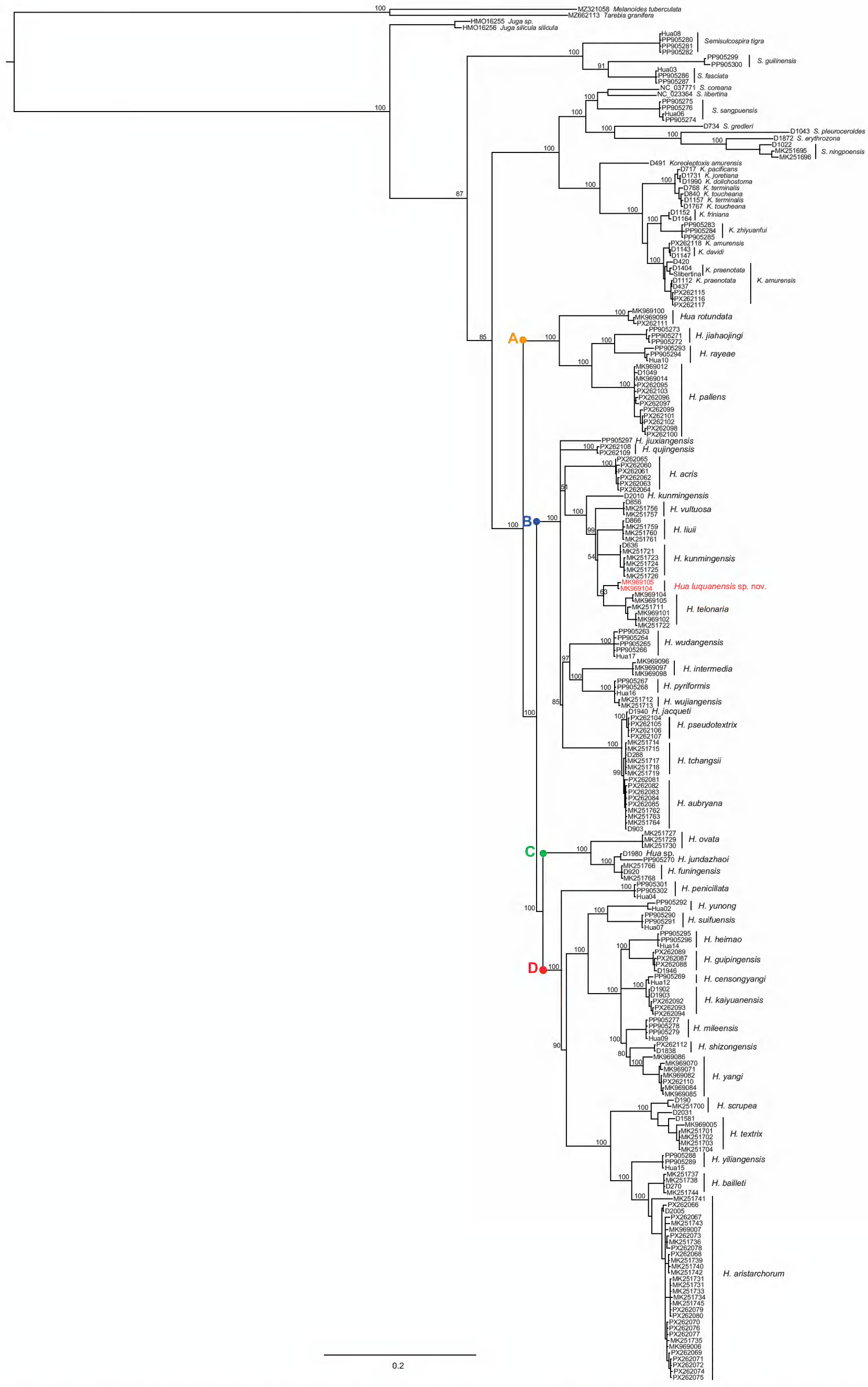

Figure 2. Maximum likelihood phylogram of *Hua* based on concatenated analysis of 13 mitochondrial protein-coding genes and COI sequences. Sequence labels are GenBank accession numbers or lab codes (prefixes Hua/D for new mitochondrial genomes from this study) followed by species names. Numbers at nodes represent ultrafast bootstrap support values, with only values above 50% shown.

showed that the average uncorrected p-distance between the new species and its closely related congeners ranged from 3.7% to 5.4% (Suppl. material 1: table S2).

Systematics

Family Semisulcospiridae Morrison

Genus *Hua* Chen, 1943

Hua Chen, 1943, pp. 19–21 (type species: *Melania telonaria* Heude, 1889, by original designation); Xu 2007, pp. 1–8; Strong and Köhler 2009, pp. 483–502; Du et al. 2019a, pp. 541–551; Du et al. 2019b, pp. 825–848.

Hua luquanensis sp. nov.

https://zoobank.org/65EC4D3D-A6CB-432E-A17B-3D40F7D6DCE1

Figs 3–5

Diagnosis. Shell small to medium, smooth, conical or oval, with or without color band, shell with 4–6 whorls. Outer marginal teeth with 14 denticles, radula moderately long and coined, rhachidian broadly rectangular, wider than tall, with w-shaped lower margin and single, weakly developed basal denticle at each lower, outer corner; oviparous.

Material examined. ***Holotype.*** • KIZ014210, collected by D.-J. Kong, from Zhuanlong Dragon Spring, Zhuanlong Town, Luquan County, Kunming City, Yunnan, Jinsha River, 25°54.65'N, 102°52.55'E, on rocks, water depth about 0.1 m, in April 2017. Shell height 12.7 mm, preserved in 75% ethanol.

Paratypes. • KIZ023092–023105, same locality data as holotype, 8.8–13.4 mm H, in 75% ethanol (Table 2).

Table 2. Shell measurements of *Hua luquanensis* sp. nov.

	H	B	BW	WA	LA	N
Holotype	12.7	8.0	10.1	7.6	4.2	6
KIZ023092	11.2	7.3	9.4	7.2	3.4	5
KIZ023093	10.7	8.1	9.8	8.1	3.6	4
KIZ023094	11.0	7.3	9.5	7.4	3.6	6
KIZ023095	8.8	6.1	7.9	6. 5	3.5	5
KIZ023096	10.8	7.0	9.0	6.8	3.4	6
KIZ023097	12.4	7.6	10.2	7.3	4.0	6
KIZ023098	12.0	7.7	9.6	7.3	3.7	5
KIZ023099	9.1	6.2	7.7	5.9	3.2	5
KIZ023100	13.4	8.4	11.2	8.2	4.3	6
KIZ023101	12.8	8.3	10.9	7.8	4.2	5
KIZ023102	13.0	8.1	10.5	7.6	4.0	6
KIZ023103	11.4	7.4	9.6	6.9	3.8	5
KIZ023104	11. 9	7.9	10.0	7.2	3.5	6
KIZ023105	10.8	7.2	9.2	6.7	3.6	4

Other material. In 99% ethanol from type locality, KIZ023106–023113 were used for anatomical study.

Etymology. *Hua luquanensis* sp. nov. is named after the type location in Luquan County. An adjective. We suggest the Chinese common name as "禄劝华蜷".

Description. ***Shell*** (Fig. 3Z1) small, up to 13.4 mm, smooth, ovate, thin, yellow-brown in color, approximately four to six whorls. Apex pointed or eroded. Aperture ovate, columella and inner lip whitish blue, outer lip black.

Operculum (Fig. 3Z2) ovate, corneous, dark brown in color, with approximately four or five whorls. Nucleus located roughly lower one-third of operculum length.

External morphology (Fig. 5A). Snout, neck, sides of foot, and dorsal surfaces of tentacles grey, without pigment. Snout broad, squarish, tentacles roughly equal to snout in length (in preserved specimens). Ciliated egg

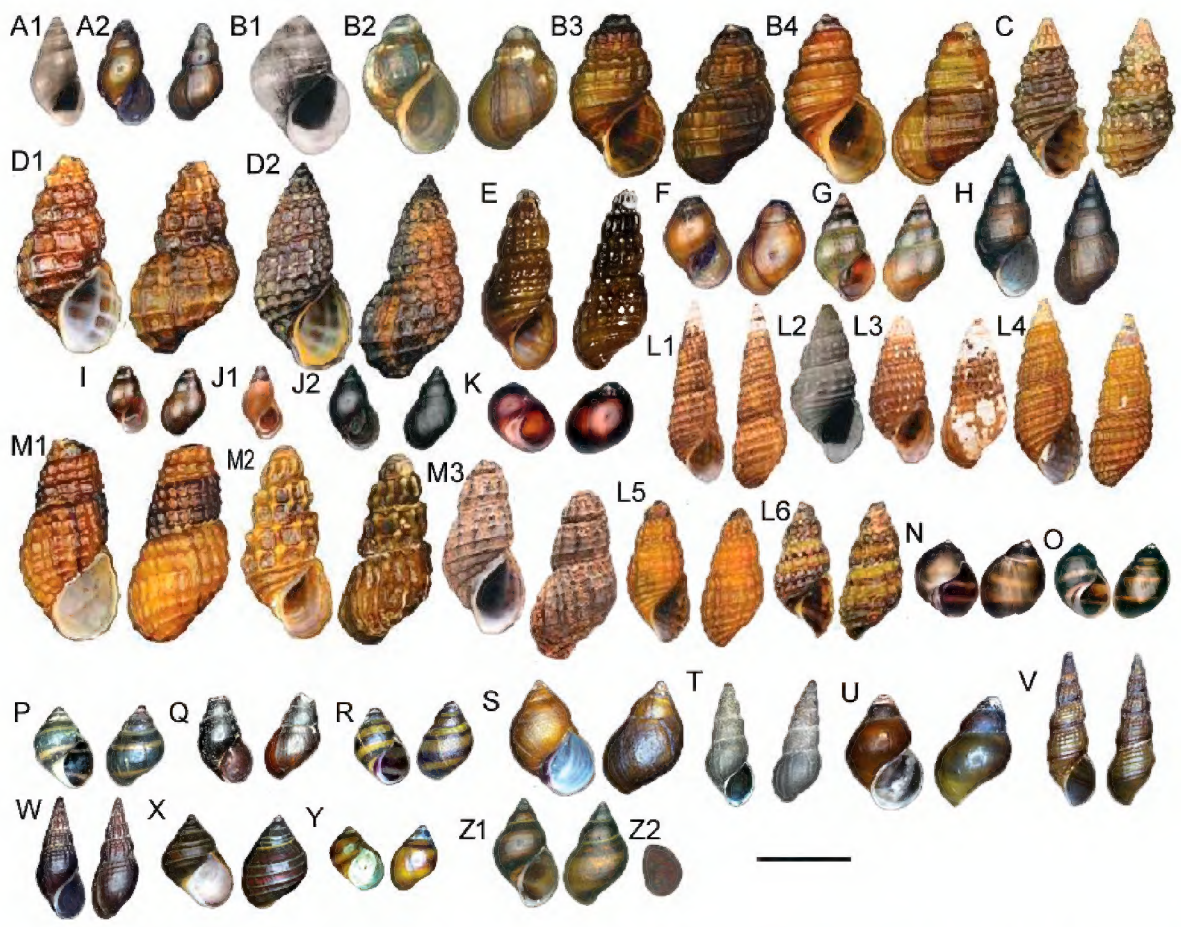

Figure 3. Shells of *Hua* species from Yunnan. **A1–A2.** *H. telonaria*; **B1–B3.** *H. aristarchorum*; **C.** *H. aubryana*; **D1–D2.** *H. bailleti*; **E.** *H. pseudotextrix*; **F.** *H. liuii*; **G.** *H. funingensis*; **H.** *H. tchangsii*; **I.** *H. kunmingensis*; **J1–J2.** *H. vultuosa*; **K.** *H. shizongensis*; **L1–L6.** *H. textrix*; **M1–M3.** *H. scrupea*; **N.** *H. qujingensis*; **O.** *H. kaiyuanensis*; **P.** *H. heimao*; **Q.** *H. dazhaoi*; **R.** *H. censongyangi*; **S.** *H. mileensis*; **T.** *H. penicillata*; **U.** *H. jiuxiangensis*; **V.** *H. suifuensis*; **W.** *H. yunong*; **X.** *H. rayeae*; **Y.** *H. yiliangensis*; **Z1.** *Hua luquanensis* sp. nov., holotype, KIZ014210; **Z2.** Operculum. Scale bar: 1 cm.

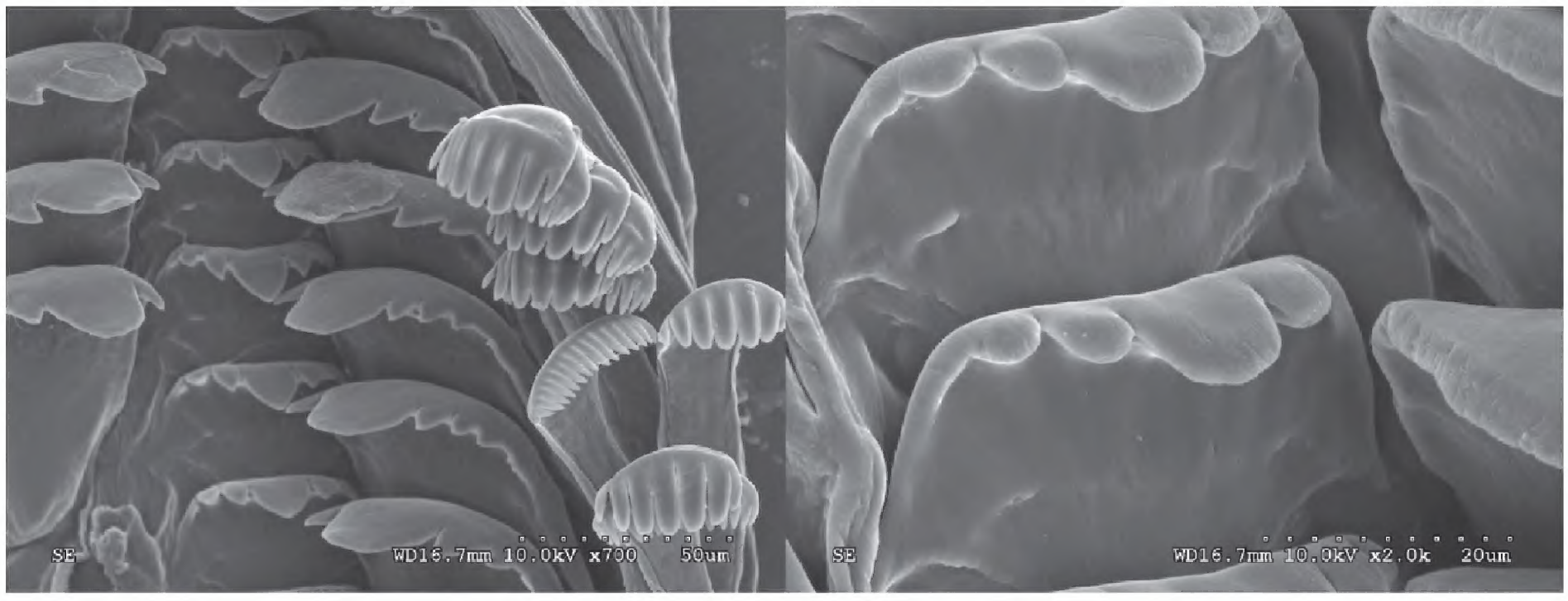

Figure 4. Radula of *Hua luquanensis* sp. nov. (Specimen: KIZ014211; Tooth types: central teeth, lateral teeth, marginal teeth).

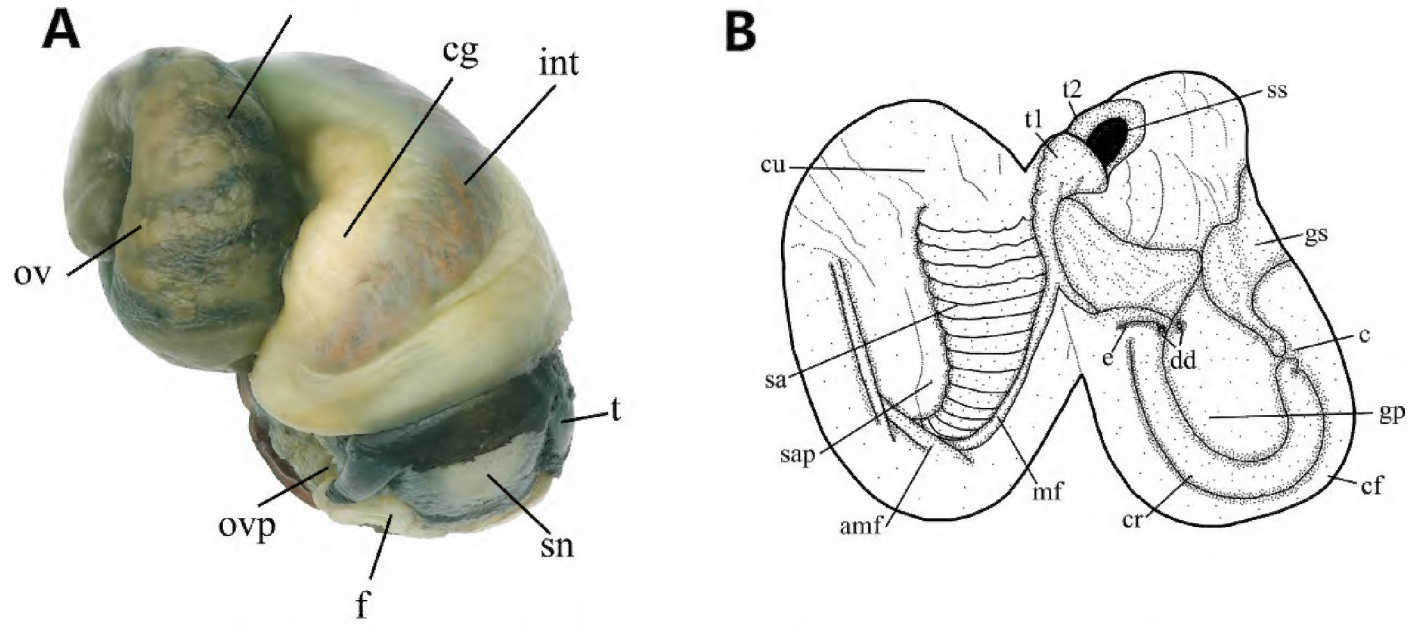

Figure 5. Anatomy of *Hua luquanensis* sp. nov. **A.** External anatomy. **B.** Midgut anatomy. Abbreviations: c, caecum; cf, caecal fold; cg, capsule gland; cr, crescentic ridge; cu, cuticularized region of stomach roof; dg, digestive gland; f, foot; gp, glandular pad; gs, gastric shield; int, intestine; mf, marginal fold; ovp, ovipositor; sa, sorting area; sap, sorting area pad; ss, lip of stale sac; sn, snout; t, cephalic tentacle; t1, major typhlosole; t2, minor typhlosole.

groove forming shallow, triangular trough between anterior tip of oviduct and ovipositor pore on side of neck below right cephalic tentacle. Ctenidium extending from posterior end of mantle cavity to near mantle edge, anterior curving toward left. Osphradium forming simple ridge along efferent branchial vessel; osphradium roughly one half of ctenidium in length. Margin of mantle smooth.

Radula (Fig. 4). Central teeth with W-shaped lower margin and single, weakly developed basal denticle at each lower and outer corner, upper margin with one large central triangular cusp, and two or three conical denticles on each side, lateral teeth with single prominent squarish cusp and three small denticles at each side, inner marginal teeth with eight and outer with fourteen denticles.

Midgut (Fig. 5B). Oesophagus opening under ledge on left side of midgut floor. Marginal fold extending anteriorly from oesophageal aperture alongside major typhlosole, then turning posteriorly bordering right margin of sorting area. Accessory marginal fold near oesophagus. Gastric shield tongue shaped and glandular pad large, rounded posteriorly, overhanging lip forming shallow pocket behind gastric shield and curving to right. Crescentic ridge bounding shallow, deep crescentic groove. Caecal fold along floor opposite and slightly behind caecum. Style sac u-shaped and in contact with intestinal groove.

Reproductive system. **Male.** Gonad dorsally surrounding digestive gland from tip of visceral mass to posterior end of midgut. Narrow vas deferens emerging ventrally from testes, continuing forward along ventral midline of whorl. Vas deferens entering posterior end of prostate at base of mantle cavity. Prostate glandular, opening to mantle cavity through narrow aperture along entire length. Glandular tissue of lateral lamina forming tall, elongate mound along posterior ventral edge. Medial lamina rather thin, forming functionally closed tube along posterior half of prostate. Dorsally and posteriorly, prostate forming flattened flange.

Female. Renal oviduct entering glandular pallial oviduct at base of mantle cavity. Pallial oviduct with proximal albumen and distal capsule glands; glands of oviduc concentrated along dorsal crest of pallial oviduct with glands forming opposing flattened surfaces bounding deep gonoductal groove. Pallial oviduct communicating with mantle cavity through narrow

aperture along entire length, except for tubular section of albumen gland at base of mantle cavity. Above aperture, along anterior half of oviduct, deep sperm gutter present within medial lamina; gutter opening to long, narrow spermatophore bursa. Behind opening to bursa, sperm gutter shallowing posteriorly, continuing to aperture of seminal receptacle just inside ventral edge of medial lamina at posterior end of pallial oviduct. Prominent glandular protuberance from ventral edge of albumen gland along opposing surface of lateral lamina extending into receptacle aperture. Sex ratio of dissected specimens: 5 females / 1 male.

Distribution and habitat. Known from Zhuanlong Dragon Spring, Zhuanlong Town, Luquan County, Kunming City, Yunnan Province, China, belonging to the Jiasha River basin. The water rises from the ground and flows into a river. The water was clear with a maximum depth of about 60 cm. River bottom substrate rocks and sand. Stonewort was the dominant macrophyte. *Hua luquanensis* sp. nov. snails were found attached to the bottom of stone (Fig. 1B).

Remarks. The outer marginal teeth with 14 denticles and the central teeth with a W-shaped lower margin of *Hua luquanensis* sp. nov. are significant distinguishing features from other *Hua* species. The new species can also be further distinguished from other *Hua* congeners by the following features: shell smooth (vs. shell sculptured in *H. aristarchorum* (Heude, 1888), *H. aubryana* (Heude, 1888), *H. bailleti* (Bavay & Dautzenberg, 1910), *H. guipingensis*, *H. jacqueti* (Dautzenberg & Fischer, 1906), *H. ovata*, *H. pseudotextrix*, *H. scrupea* (Fulton, 1914), *H. textrix* (Heude, 1888), *H. rayeae*, *H. yunong*, and *H. censongyangi*); shell with 4–6 whorls (vs. 3–4 in *H. kunmingensis* and *H. liuii*, 8–9 in *H. tchangsii* Du, Köhler, Chen & Yang, 2019, and 7–9 in *H. intermedia* (Gredler, 1885) and *H. vultuosa*); outer marginal teeth with 14 flattened denticles (vs. 8 in *H. qiannanensis*); body width about 61.4–74.8% of shell height (vs. 50.3–56.8% in *H. jacqueti* (Dautzenberg & Fischer, 1906) and 74.2–90.0% in *H. rotundata* (Heude, 1888)); a large body whorl comprising about 79.8–91.7% of shell height (vs. 68.2–75% in *H. telonaria*).

Discussion

In Asia, three semisulcospirid genera have been recorded, *Hua*, *Koreoleptoxis*, and *Semisulcospira* (Strong and Köhler 2009; Köhler 2017; Du et al. 2019a). Species of *Semisulcospira* are viviparous, while *Hua* and *Koreoleptoxis* are oviparous. Species of *Hua* can be distinguished from *Koreoleptoxis* based on the following characteristics: mature females of *Hua* possess only an oviparous pore on the side of the neck below the right cephalic tentacle (vs. female with both an oviparous pore and an egg-laying groove), and the inner and outer marginal teeth of the radula have a different number of denticles (vs. the same number of denticles) (Du et al. 2019a).

The new species is here assigned to the genus *Hua*, as it possesses features typical of *Hua*, i.e., a shell smooth, oviparous, a mature female with an oviparous pore on the side of the neck below the right cephalic tentacle, and inner and outer marginal teeth with a different number of denticles. This assignment is supported by the molecular data, which indicate that *Hua luquanensis* sp. nov. is nested in the genus *Hua* with high support values. The observed p-distances of the COI gene between *Hua luquanensis* sp. nov. and its congeners range from 4.1% to 13.1% (with an average of 10.3%). Coupled with the considerable geographical separation and morphological differences from its congeners, this supports its status as a distinct and valid species. A total of 26 species of the genus *Hua* have now been recorded in Yunnan Province (including *Hua luquanensis* sp. nov.). The discovery of this and other recently described species adds to the growing recognition of Yunnan's karst landscapes as biodiversity hotspots, where isolated aquatic habitats drive high rates of endemism in gastropods (Chen 2013; Yang et al. 2016).

Du and Yang (2023) identified four major clades within the genus *Hua* based on Bayesian inference (BI) analysis of combined 16S rRNA and COI data. However, due to low support values at key nodes, the phylogenetic relationships among these four clades remained unresolved. In this study, the maximum-likelihood tree constructed from combined COI and mitogenome data obtained high support values and further clarified the phylogenetic relationships within the genus *Hua*. The genus *Hua* is divided into four major clades with distinct species groups: Clade A includes four species, *H. rotundata*, *H. jiahaozhangi*, *H. rayeae*, and *H. pallens*; Clade B includes 15 species, namely *H. qujingensis*, *H. jiuxiangensis*, *H. acris*, *H. kunmingensis*, *H. vultuosa*, *H. liuii*, *H. luquanensis* sp. nov., *H. telonaria*, *H. wudangensis*, *H. intermedia*, *H. pyriformis*, *H. wujiangensis*, *H. jacqueti*, *H. pseudotextrix*, *H. tchangsii*, and *H. aubryana*; Clade C contains three species, namely *H. ovata*, *H. jundazhaoi*, and *H. funingensis* Du, Köhler, Chen & Yang, 2019; Clade D contains 15 species, namely *H. penicillata*, *H. yunong*, *H. suifuensis*, *H. heimao*, *H. guipingensis*, *H. censongyangi*, *H. kaiyuanensis*, *H. mileensis*, *H. yangi*, *H. scrupea*, *H. textrix*, *H. yiliangensis*, *H. bailleti*, *H. aristarchorum*, and *H. shizongensis*.

Despite this notable diversity, many Semisulcospiridae species are facing severe survival threats. With environmental pollution and waterway development, several species have disappeared due to eutrophication. The habitat of *Hua luquanensis* sp. nov. was destroyed in 2018 due to a private home being built on the creek. Therefore, we hope this paper will inspire conservation efforts to value and protect the ecological environment and other species. To mitigate further biodiversity loss, urgent actions such as habitat restoration, legal protection of spring ecosystems, and community-based conservation programs should be prioritized in Luquan County and similar regions.

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References

Chen SF (1943) Two new genera, two new species and two new names of Chinese Melaniidae. The Nautilus 57: 19–21. https://biostor.org/reference/131593

Chen XY (2013) Checklist of Fishes of Yunnan. Zoological Research 34: 281–343. https://doi.org/10.11813/j.issn.0254-5853.2013.4.0281

Chen H, Shi BY, Du LN, Sun HY (2023) Description of a New Species of *Hua* (Gastropoda: Semisulcospiridae) from Guizhou, China, Based on Morphology and Molecular Evidence. Zoological Science 40(5): 414–421. https://doi.org/10.2108/zs230025

Du LN, Yang JX (2023) Semisulcospiridae Morrison, 1952. In: Du LN, Yang JX (Eds) Colored Atlas of Chinese Melania. Henan Science and Technology Press, Zhengzhou. [in Chinese]

Du LN, Yang JX, Köhler F, Yu GH, Chen XY (2019a) Comparative morpho-anatomy and mitochondrial phylogeny of Semisulcospiridae in Yunnan, south-western China, with description of four new species (Gastropoda: Cerithioidea). Invertebrate Systematics 33(6): 825–848. https://doi.org/10.1071/IS18084

Du LN, Chen J, Yu GH, Yang JX (2019b) Systematic relationships of Chinese freshwater semisulcospirids (Gastropoda, Cerithioidea) revealed by mitochondrial sequences. Zoological Research 40(6): 541–551. https://doi.org/10.24272/j.issn.2095-8137.2019.033

He YM, Lu YZ, Fu ZY, Xiang HQ, Chen H (2024) Description of 17 new species of Semisulcospiridae (Gastropoda: Cerithioidea) from southern China based on morphological and molecular evidence. Ecologica Montenegrina 75: 12–32. https://doi.org/10.37828/em.2024.75.2

Holznagel WE (1998) A non-destructive method for cleaning gastropod radulae from frozen, alcohol-fixed, or dried material. American Malacological Bulletin 14: 181–183.Katoh K, Standley DM (2013) MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Molecular Biology and Evolution 30(4): 772–780. https://doi.org/10.1093/molbev/mst010

Katoh K, Standley DM (2013) MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Molecular Biology and Evolution 30(4):772–780. https://doi.org/10.1093/molbev/mst010

Köhler F (2017) Against the odds of unusual mtDNA inheritance, introgressive hybridization and phenotypic plasticity: Systematic revision of Korean freshwater gastropods (Semisulcospiridae, Cerithioidea). Invertebrate Systematics 31: 249–268. https://doi.org/10.1071/IS16077

Kumar S, Stecher G, Tamura K (2016) MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. Molecular Biology and Evolution 33: 1870–1874. https://doi.org/10.1093/molbev/msw054

Lanfear R, Frandsen PB, Wright AM, Senfeld T, Calcott B (2017) PartitionFinder 2: New Methods for Selecting Partitioned Models of Evolution for Molecular and Morphological Phylogenetic Analyses. Molecular Biology and Evolution 34(3): 772–773. https://doi.org/10.1093/molbev/msw260

Minh BQ, Nguyen MA, von Haeseler A (2013) Ultrafast approximation for phylogenetic bootstrap. Molecular Biology and Evolution 30(5): 1188–1195. https://doi.org/10.1093/molbev/mst024

Morrison JPE (1954) The relationships of old and new world melanians. Proceedings of the United States National Museum 103: 357–394. https://doi.org/10.5479/SI.00963801.103-3325.357

Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ (2015) IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Molecular Biology and Evolution 32(1): 268–274. https://doi.org/10.1093/molbev/msu300

Palumi SR, Martin A, Romano S, McMillan WO, Stice L, Grabowski G (1991) The simple fool's guide to PCR. University of Hawaii, Honolulu.

Posada D (2008) jModelTest: Phylogenetic model averaging. Molecular Biology and Evolution 25: 1253–1256.

Strong EE, Köhler F (2009) Morphological and molecular analysis of '*Melania*' *jacqueti* Dautzenberg and Fischer, 1906: from anonymous orphan to critical basal offshoot of the Semisulcospiridae (Gastropoda: Cerithioidea). Zoologica Scripta 38: 483–502. https://doi.org/10.1111/j.1463-6409.2008.00385.x

Xu XF (2007) Classification and Morphology on Pleuroceridae (Gastropoda: Mesogastropoda) of some area in middle reaches of Changjiang River. PhD thesis, Nancang University, China.

Yang HF, Li WX, Chen ZM (2016) A new cave species of the genus *Triplophysa* from Yunnan, China. Zoological Research 37: 296–300. https://doi.org/10.13918/j.issn.2095-8137.2016.5.296

Supplementary material 1

Supplementary information

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Data type: docx

Explanation note: **table S1**. Sequenced material. Voucher numbers, localities, and GenBank accession numbers. **table S2**. Genetic distance (uncorrected *p*-distances) for COI between Chinese semisulcospirids.

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